ENTERED

```
      RAW SEQUENCE LISTING                  DATE: 04/23/2001
      PATENT APPLICATION:  US/09/832,320    TIME: 13:21:16

      Input Set : A:\Seqlist.txt
      Output Set: N:\CRF3\04232001\I832320.raw

  4 <110> APPLICANT: Crane, Edmund H.
  5         Crane, Virginia C.
  7 <120> TITLE OF INVENTION: Maize Pathogenesis-Related
  8         Polynucleotide and Methods of Use
 10 <130> FILE REFERENCE: 35718/214291
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/832,320
C--> 12 <141> CURRENT FILING DATE: 2001-04-10
 12 <150> PRIOR APPLICATION NUMBER: US 60/195,801
 13 <151> PRIOR FILING DATE: 2000-04-10
 15 <160> NUMBER OF SEQ ID NOS: 3
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 898
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Zea mays
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (63)...(674)
 28 <400> SEQUENCE: 1
 29 ctcgcacgca ctcgacgctc attcactgag ccatttactc agatcaccaa ctccagatct      60
 30 ca'atg gcg cac tcg cgc agc cac cac cac ctc ctc ctg ctc ccc gcg         107
 31     Met Ala His Ser Arg Ser His His His Leu Leu Leu Leu Pro Ala
 32     1               5                   10                  15
 34 ccc atg gcc acg gcg tgc ttg ctc ctc gcc acc ctc ctc gcg ctc tgc       155
 35 Pro Met Ala Thr Ala Cys Leu Leu Leu Ala Thr Leu Leu Ala Leu Cys
 36                 20                  25                  30
 38 gcc gcg ccg gcg ccg acc cac ggc gcg cgc gtc ctc atg ccg ggc ggc       203
 39 Ala Ala Pro Ala Pro Thr His Gly Ala Arg Val Leu Met Pro Gly Gly
 40             35                  40                  45
 42 gcg ggc gcg gtg acc aag gcg cag cag ggt ggc acc ggc agc ggc agc       251
 43 Ala Gly Ala Val Thr Lys Ala Gln Gln Gly Gly Thr Gly Ser Gly Ser
 44         50                  55                  60
 46 aac gcg acg gcg gac gag tac ctg gcg ccg cac aac cag gcg cgc gcg       299
 47 Asn Ala Thr Ala Asp Glu Tyr Leu Ala Pro His Asn Gln Ala Arg Ala
 48     65                  70                  75
 50 gcg gtg ggc gtg gcc ccg ctg cgg tgg aac gcg ggc ctg gct tcg gcg       347
 51 Ala Val Gly Val Ala Pro Leu Arg Trp Asn Ala Gly Leu Ala Ser Ala
 52 80                  85                  90                  95
 54 gcc gcg ggg acg gtg gcg cag cag cgg cgg cag ggc ggg tgc gcg ttc       395
 55 Ala Ala Gly Thr Val Ala Gln Gln Arg Arg Gln Gly Gly Cys Ala Phe
 56             100                 105                 110
 58 gcg gac gtg ggg gcc agc ccc tac ggc gcg aac cag ggg tgg gcg agc       443
 59 Ala Asp Val Gly Ala Ser Pro Tyr Gly Ala Asn Gln Gly Trp Ala Ser
 60             115                 120                 125
 62 tac cgc gcg cgc ccc gcc gag gtg gtg gcg ctg tgg gtg gcg gag ggg       491
 63 Tyr Arg Ala Arg Pro Ala Glu Val Val Ala Leu Trp Val Ala Glu Gly
 64         130                 135                 140
```

RAW SEQUENCE LISTING   DATE: 04/23/2001
PATENT APPLICATION: US/09/832,320   TIME: 13:21:16

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\04232001\I832320.raw

```
66 cgg tac tac acc cac gcc aac aac acg tgc gcc gcg ggg cgg cag tgc      539
67 Arg Tyr Tyr Thr His Ala Asn Asn Thr Cys Ala Ala Gly Arg Gln Cys
68     145             150             155
70 ggc acg tac acg cag gtg gtg tgg cgc aac acc gcc gag gtc ggg tgc      587
71 Gly Thr Tyr Thr Gln Val Val Trp Arg Asn Thr Ala Glu Val Gly Cys
72 160             165             170             175
74 gcg cag gcc agc tgc gcc acg ggc gcc acg ctc acg ctc tgc ctg tac      635
75 Ala Gln Ala Ser Cys Ala Thr Gly Ala Thr Leu Thr Leu Cys Leu Tyr
76             180             185             190
78 aac ccg cac ggc aac gtg cag ggc cag agc ccc tac tag ctagctgagg      684
79 Asn Pro His Gly Asn Val Gln Gly Gln Ser Pro Tyr  *
80             195             200
82 tcatcaggtc gtagcgacgg agcccaactg ccgccgccgg cggcagcgga gtacgtaggt    744
83 tcatcagtct tctctagttc ggtcacggaa aggctgtttt gtggtgtgat ccggtggtgt    804
84 tcttggtgtt gttgacaact gctttggttt ggtgtatcag cttttgttgc cgggtaaaaa    864
85 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa                                 898
87 <210> SEQ ID NO: 2
88 <211> LENGTH: 203
89 <212> TYPE: PRT
90 <213> ORGANISM: Zea mays
92 <400> SEQUENCE: 2
93 Met Ala His Ser Arg Ser His His His Leu Leu Leu Leu Pro Ala Pro
94 1               5               10              15
95 Met Ala Thr Ala Cys Leu Leu Leu Ala Thr Leu Leu Ala Leu Cys Ala
96             20              25              30
97 Ala Pro Ala Pro Thr His Gly Ala Arg Val Leu Met Pro Gly Gly Ala
98         35              40              45
99 Gly Ala Val Thr Lys Ala Gln Gln Gly Gly Thr Gly Ser Gly Ser Asn
100     50              55              60
101 Ala Thr Ala Asp Glu Tyr Leu Ala Pro His Asn Gln Ala Arg Ala Ala
102 65              70              75              80
103 Val Gly Val Ala Pro Leu Arg Trp Asn Ala Gly Leu Ala Ser Ala Ala
104             85              90              95
105 Ala Gly Thr Val Ala Gln Gln Arg Arg Gln Gly Gly Cys Ala Phe Ala
106             100             105             110
107 Asp Val Gly Ala Ser Pro Tyr Gly Ala Asn Gln Gly Trp Ala Ser Tyr
108         115             120             125
109 Arg Ala Arg Pro Ala Glu Val Val Ala Leu Trp Val Ala Glu Gly Arg
110     130             135             140
111 Tyr Tyr Thr His Ala Asn Asn Thr Cys Ala Ala Gly Arg Gln Cys Gly
112 145             150             155             160
113 Thr Tyr Thr Gln Val Val Trp Arg Asn Thr Ala Glu Val Gly Cys Ala
114             165             170             175
115 Gln Ala Ser Cys Ala Thr Gly Ala Thr Leu Thr Leu Cys Leu Tyr Asn
116             180             185             190
117 Pro His Gly Asn Val Gln Gly Gln Ser Pro Tyr
118     195             200
120 <210> SEQ ID NO: 3
121 <211> LENGTH: 612
```

RAW SEQUENCE LISTING   DATE: 04/23/2001
PATENT APPLICATION: US/09/832,320   TIME: 13:21:16

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\04232001\I832320.raw

```
122 <212> TYPE: DNA
123 <213> ORGANISM: Zea mays
125 <220> FEATURE:
126 <221> NAME/KEY: CDS
127 <222> LOCATION: (1)...(612)
129 <400> SEQUENCE: 3
130 atg gcg cac tcg cgc agc cac cac cac ctc ctc ctg ctc ccc gcg ccc      48
131 Met Ala His Ser Arg Ser His His His Leu Leu Leu Leu Pro Ala Pro
132 1               5                   10                  15
134 atg gcc acg gcg tgc ttg ctc ctc gcc acc ctc ctc gcg ctc tgc gcc      96
135 Met Ala Thr Ala Cys Leu Leu Leu Ala Thr Leu Leu Ala Leu Cys Ala
136             20                  25                  30
138 gcg ccg gcg ccg acc cac ggc gcg cgc gtc ctc atg ccg ggc ggc gcg     144
139 Ala Pro Ala Pro Thr His Gly Ala Arg Val Leu Met Pro Gly Gly Ala
140             35                  40                  45
142 ggc gcg gtg acc aag gcg cag cag ggt ggc acc ggc agc ggc agc aac     192
143 Gly Ala Val Thr Lys Ala Gln Gln Gly Gly Thr Gly Ser Gly Ser Asn
144         50                  55                  60
146 gcg acg gcg gac gag tac ctg gcg ccg cac aac cag gcg cgc gcg gcg     240
147 Ala Thr Ala Asp Glu Tyr Leu Ala Pro His Asn Gln Ala Arg Ala Ala
148 65                  70                  75                  80
150 gtg ggc gtg gcc ccg ctg cgg tgg aac gcg ggc ctg gct tcg gcg gcc     288
151 Val Gly Val Ala Pro Leu Arg Trp Asn Ala Gly Leu Ala Ser Ala Ala
152                 85                  90                  95
154 gcg ggg acg gtg gcg cag cag cgg cgg cag ggc ggg tgc gcg ttc gcg     336
155 Ala Gly Thr Val Ala Gln Gln Arg Arg Gln Gly Gly Cys Ala Phe Ala
156             100                 105                 110
158 gac gtg ggg gcc agc ccc tac ggc gcg aac cag ggg tgg gcg agc tac     384
159 Asp Val Gly Ala Ser Pro Tyr Gly Ala Asn Gln Gly Trp Ala Ser Tyr
160             115                 120                 125
162 cgc gcg cgc ccc gcc gag gtg gtg gcg ctg tgg gtg gcg gag ggg cgg     432
163 Arg Ala Arg Pro Ala Glu Val Val Ala Leu Trp Val Ala Glu Gly Arg
164         130                 135                 140
166 tac tac acc cac gcc aac aac acg tgc gcc gcg ggg cgg cag tgc ggc     480
167 Tyr Tyr Thr His Ala Asn Asn Thr Cys Ala Ala Gly Arg Gln Cys Gly
168 145                 150                 155                 160
170 acg tac acg cag gtg gtg tgg cgc aac acc gcc gag gtc ggg tgc gcg     528
171 Thr Tyr Thr Gln Val Val Trp Arg Asn Thr Ala Glu Val Gly Cys Ala
172                 165                 170                 175
174 cag gcc agc tgc gcc acg ggc gcc acg ctc acg ctc tgc ctg tac aac     576
175 Gln Ala Ser Cys Ala Thr Gly Ala Thr Leu Thr Leu Cys Leu Tyr Asn
176             180                 185                 190
178 ccg cac ggc aac gtg cag ggc cag agc ccc tac tag                     612
179 Pro His Gly Asn Val Gln Gly Gln Ser Pro Tyr *
180         195                 200
```

VERIFICATION SUMMARY   DATE: 04/23/2001
PATENT APPLICATION: US/09/832,320   TIME: 13:21:17

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\04232001\I832320.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date